

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/913,569

DATE: 02/25/2002
TIME: 10:16:47



Input Set : A:\BB1344 Seq List.txt
Output Set: N:\CRF3\02252002\I913569.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1 ✓
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 ✓
L:72 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2 ✓
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 ✓
L:223 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7 ✓
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 ✓
L:224 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7 ✓
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 ✓
L:573 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17 ✓
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 ✓
L:608 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18 ✓
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 ✓
L:636 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19 ✓
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 ✓
L:637 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19 ✓
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 ✓
L:677 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20 ✓
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 ✓
L:680 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20 ✓
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 ✓
L:1054 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33 ✓
L:1054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 ✓
L:1093 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34 ✓
L:1093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 ✓
L:1148 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35 ✓
L:1148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 ✓
L:1149 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35 ✓
L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 ✓
L:1150 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35 ✓
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 ✓
L:1151 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35 ✓
L:1151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 ✓
L:1184 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:36 ✓
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 ✓
L:1207 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:37 ✓
L:1207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 ✓
L:1289 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:41 ✓
L:1289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 ✓
L:1292 M:214 E: (33) Seq.# missing, SEQ ID NO:42
L:1316 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:43 ✓
L:1316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 ✓
L:1317 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:43 ✓
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 ✓
L:1340 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:44 ✓
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 ✓
L:1409 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45 ✓



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Input Set : A:\BB1344 Seq List.txt
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L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1410 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45
L:1410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1411 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45
L:1411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45
L:1412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45
L:1413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1414 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45
L:1414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1438 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
L:1438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1462 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:47
L:1462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1465 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:47
L:1465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1488 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
L:1488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1491 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
L:1491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1494 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
L:1494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1559 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:1559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1562 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:1562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1564 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:1564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1565 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:1565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1616 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1617 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
L:1617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1618 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
L:1618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1675 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:55
L:1675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1676 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:55
L:1676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1677 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:55
L:1677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:15 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (56) Counted (55)



SEQUENCE LISTING

<110> Krebbers, Enno
Weng, Zude
Cahoon, Rebecca

<120> Plant Viral Movement Protein Genes

<130> BB1344

<140> 09/913,569

<141> 2001-12-17

<150> 60/128,092

<151> 1999-04-07

<160> 56

<170> Microsoft Office 97

<210> 1

<211> 450

<212> DNA

<213> Vitis sp.

<220>

<221> unsure

<222> (445)

<223> n = A, C, G or T

<400> 1

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atgcctcaag	gaacacttga	agtccttctt	gtcagtgcc	agggctctga	gaacactgat	120
tttctctgta	acatggatcc	ttatgttggt	ctcacttgcc	gcactcagga	gcagaaaagc	180
agtgttgcat	caggaaaagg	gtctgaccca	gaatggaatg	aacattttgt	attcaccata	240
tctgaaggca	tctcagaact	caccattaaa	ataatggaca	gtgatagcgg	tagtggtgat	300
gattttgtgg	gagaagcaac	cattccacta	gaggcactct	tcacggaagg	aagcctggag	360
ccaagcaccg	gtacaatgtt	gttaaagacc	aaggaatatt	gtggagagat	taaagttggc	420
ctcactttca	ctcaaaagg	aaaangtgat				450

<210> 2

<211> 130

<212> PRT

<213> Vitis sp.

<220>

<221> UNSURE

<222> (129)

<223> Xaa = any amino acid

<400> 2

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Glu	Asn	Thr	Asp	Phe	Leu	Cys	Asn	Met	Asp	Pro	Tyr	Val	Val	Leu	Thr
			20					25						30	
Cys	Arg	Thr	Gln	Glu	Gln	Lys	Ser	Ser	Val	Ala	Ser	Gly	Lys	Gly	Ser
		35					40					45			
Asp	Pro	Glu	Trp	Asn	Glu	His	Phe	Val	Phe	Thr	Ile	Ser	Glu	Gly	Ile
		50				55					60				
Ser	Glu	Leu	Thr	Ile	Lys	Ile	Met	Asp	Ser	Asp	Ser	Gly	Ser	Gly	Asp
		65			70				75						80

Asp Phe Val Gly Glu Ala Thr Ile Pro Leu Glu Ala Leu Phe Thr Glu
85 90 95

Gly Ser Leu Glu Pro Ser Thr Gly Thr Met Leu Leu Lys Thr Lys Glu
100 105 110

Tyr Cys Gly Glu Ile Lys Val Gly Leu Thr Phe Thr Gln Lys Gly Lys
115 120 125

Xaa Asp
130

<210> 3
<211> 916
<212> DNA
<213> Zea mays

<400> 3
gcacgagcac gccgcctcca tgtgggtggg gaggcaaacg cgttcgtcca tctctgaaac 60
tcaaacgcct tgtattggag catactacag gagtacttct gtacaaatat aaataccocct 120
ggcgagttgg gttgggtcta tctcgcaatc gaggcgtttt ttttctgctt cgtaagttcg 180
tggtcgatcc agcgagcgag cgagcagacc ggcggctaac cgcggaggga gagatggcgc 240
aggggacgct ggaggtgctt ctcgctggag ccaggggcct cgagaacacc gattacctga 300
gcaacatgga cccctacgag cttctgcaat gtcgctccca cgagcagaag agcagcgctcg 360
catctggcaa aggctgtgaa cctgagtggg acgagacctt cgtgttcacc gtctccgatg 420
gcgcgacaga gctgttcata aagctcctgg acagtgacgg tggcactgat gacgattttg 480
ttggtgaggg aacgattcct ctggaagcag tttacacgga aggaaacatc cctccgactg 540
tttacaatgt tgtgaaagac gaagaatacc gcgagagaaat caaagttggc ctcacgttca 600
ctccagagga ccagggcttc tgaggaataa cttggcggtgt ggccgctgga actggaggca 660
gcaggcagtc gtcttatgat tcagaagcaa acgacggatc gattcccttg atgtactgca 720
gtccagtggag cgtgcatacta caactttag aagaagcctg caacatgatc acgggatcct 780
gtactgcatc actctaaagc ctagctaaaa ccaccagctc ctgtacttga tgccgggcgg 840
gcttgtcatg tactgaaacc tacaataacg gtcgccgaac cccactcttt gatgttaaaa 900
aaaaaaaaa aaaaaa 916

<210> 4
<211> 129
<212> PRT
<213> Zea mays

<400> 4
Met Ala Gln Gly Thr Leu Glu Val Leu Leu Val Gly Ala Arg Gly Leu
1 5 10 15

Glu Asn Thr Asp Tyr Leu Ser Asn Met Asp Pro Tyr Ala Leu Leu Gln
20 25 30

Cys Arg Ser His Glu Gln Lys Ser Ser Val Ala Ser Gly Lys Gly Cys
35 40 45

Glu Pro Glu Trp Asn Glu Thr Phe Val Phe Thr Val Ser Asp Gly Ala
50 55 60

Ala Glu Leu Phe Ile Lys Leu Leu Asp Ser Asp Gly Gly Thr Asp Asp
65 70 75 80

Asp Phe Val Gly Glu Ala Thr Ile Pro Leu Glu Ala Val Tyr Thr Glu
85 90 95

Gly Asn Ile Pro Pro Thr Val Tyr Asn Val Val Lys Asp Glu Glu Tyr
100 105 110

Arg Gly Glu Ile Lys Val Gly Leu Thr Phe Thr Pro Glu Asp Gln Gly
115 120 125

Phe

<210> 5
<211> 876
<212> DNA
<213> Zea mays

<400> 5
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ggaggaggac atggtgcacg ggacgctgga agtgctgctc gttggggcca agggcctcga 120
gaacaccgat tacctctgta acatggatcc gtatgcaatt ctcaagtgcc gttcacagga 180
gcagaagagc agtattgcaa ctggaaaagg aactaccctt gagtggaatg aaaactttat 240
cttcactgtg tctgaccgga caacagactt ggtaatcaag cttatggaca gtgatacagg 300
cacagcagat gactttgttg gtgaagcaac gattccattg gaagcagtgt atactgaaag 360
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attcatgcgc ttggagcctt cagccgtcga gtacttcatt ctaatgcaga attcattcga 600
tttggttctt tttgattgtt tcagaagaag tggtattagt gagtttcaac aaaaaatagc 660
tccatattgc tctatatccc gtattggaaa ttctaaggcc gtttgtgatt actgcttaca 720
acaagaagtt ttgcttctag ttcccactac gctttttttt gaagttttga gtggaacatc 780
tttgtgttca acgtttgggg aggtgtaggc cagtaatact gcaagaaagg aataatttcc 840
cttgcagcaa cattgttttt tgtgatcctt gaaaaa 876

<210> 6
<211> 143
<212> PRT
<213> Zea mays

<400> 6
Met Val His Gly Thr Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu
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Glu Asn Thr Asp Tyr Leu Cys Asn Met Asp Pro Tyr Ala Ile Leu Lys
20 25 30
Cys Arg Ser Gln Glu Gln Lys Ser Ser Ile Ala Thr Gly Lys Gly Thr
35 40 45
Thr Pro Glu Trp Asn Glu Asn Phe Ile Phe Thr Val Ser Asp Arg Thr
50 55 60
Thr Asp Leu Val Ile Lys Leu Met Asp Ser Asp Thr Gly Thr Ala Asp
65 70 75 80
Asp Phe Val Gly Glu Ala Thr Ile Pro Leu Glu Ala Val Tyr Thr Glu
85 90 95
Arg Ser Ile Pro Pro Thr Leu Tyr Asn Val Val Lys Gly Glu Lys Tyr
100 105 110
Cys Gly Glu Ile Lys Val Gly Leu Thr Phe Thr Pro Glu Asp Thr Arg
115 120 125
Gln Arg Gly Leu Pro Glu Asp Phe Gly Gly Trp Lys Gln Ser Ser
130 135 140

<210> 7
<211> 771
<212> DNA
<213> Hevea brasiliensis

<220>
<221> unsure
<222> (671)
<223> n = A, C, G or T

<220>
 <221> unsure
 <222> (721)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (752)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (767)
 <223> n = A, C, G or T

<220>
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 <222> (769)
 <223> n = A, C, G or T

<400> 7
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 cacagatacc caaagggcag agatccaaga actcatttca atctaaattc ctgttgagtt 120
 ttaagtcttt tctttttcgc tttttggatt caattctggt ccaaaaaatgc ctctaggaac 180
 tgttgaagtc ctacttggtg gtgctaaggg tcttgaaaac actgattttc tcaatggcgt 240
 ggacccttat gtcgtcctcg cttgccgtac ccaggagcag aaaagcagtg ttgcttcagg 300
 gaaagggagt gaaccagaat ggaatgagaa attctcattt gaggtatcag atggtgacac 360
 agaactcaca ttgaaaatca tggacagtga tgttggtgct gcagatgatt ttgttggaga 420
 agcaaccatt ccccttgagc cattgttttt ggaaggaaaac ctcccatacta cggcgtacaa 480
 agttgtcaaa gaacaagaat acaagggaga gattacagtg ggcctcacct tcaccccaga 540
 ggtagagatg gacaacgtcg gagtggatgg atacgatttt cgggttataat attaactagc 600
 atcttgggtg ggaaatggca aggactgctt ttggtttggga gatggcaaaa gagactccgt 660
 ttttaacgtc natgttgttg ttgaaaactt ggtttttgat gtttgcaaaa aatacccgat 720
 nttgttttaa agaaaccctt tttggggggt tngaaattga atttggnant t 771

<210> 8
 <211> 140
 <212> PRT
 <213> Hevea brasiliensis

<400> 8
 Met Pro Leu Gly Thr Val Glu Val Leu Leu Val Gly Ala Lys Gly Leu
 1 5 10 15
 Glu Asn Thr Asp Phe Leu Asn Gly Val Asp Pro Tyr Val Val Leu Ala
 20 25 30
 Cys Arg Thr Gln Glu Gln Lys Ser Ser Val Ala Ser Gly Lys Gly Ser
 35 40 45
 Glu Pro Glu Trp Asn Glu Lys Phe Ser Phe Glu Val Ser Asp Gly Asp
 50 55 60
 Thr Glu Leu Thr Leu Lys Ile Met Asp Ser Asp Val Gly Ala Ala Asp
 65 70 75 80
 Asp Phe Val Gly Glu Ala Thr Ile Pro Leu Glu Pro Leu Phe Leu Glu
 85 90 95
 Gly Asn Leu Pro Ser Thr Ala Tyr Lys Val Val Lys Glu Gln Glu Tyr
 100 105 110
 Lys Gly Glu Ile Thr Val Gly Leu Thr Phe Thr Pro Glu Val Glu Met
 115 120 125

Asp Asn Val Gly Val Asp Gly Tyr Asp Phe Arg Leu
130 135 140

<210> 9
<211> 874
<212> DNA
<213> Triticum aestivum

<400> 9
gcacgaggcc gagctttcca tttttcaact cctagtccta tacatacagc ggaacccccg 60
ggctcggatc ggatctacag caattagtct cgaccttcag tcgtgccgcc tgctcatcag 120
catataattc ctgatcgagc gagcgggaga ggaaggcgag atcaggcccg gagagaagat 180
ggcgcagggg acgctggagg tgctgctcgt gggagccaag ggccctcgaga acaccgacta 240
cctctgcaac atggaccggt acgcggttct aaaatgcacc tcgcaggagc aaaagagcac 300
cgtcgcctct ggaaagggaa gtgatcctga gtggaacgaa accttttgtt tcaccgtctc 360
tgagaatgca actgagcttg tcatcaagct actggacagt gatggtggca cggacgacga 420
cagcgttggt gaagcaacga tcccattgga tggagtgtac actgaaggaa gcatcccacc 480
aactgtttac aatgttgta aagacgaaga gtaccgtgga gaaatcaaaa ttggtctgac 540
gttcactccg gaggaggctc gtgatcagga tcaaccogag gaaaactatg gtgggtggaa 600
ccaatcatct tgagaagaag caggtgcttt gctgaactat ggtgcgtgac aagtcgtgtg 660
ctagaactaa agcctatatt aattgttaaa gactgtattt gtcgttgatt cctcaatta 720
tggaatagct acgaatctac ttattgattg gtatcgtttt ctaatattca aatttgtaat 780
aacagtgttc cccacttgta tgaagtatga gcctctttaa tgtaactaaa ctgagttgca 840
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 874

<210> 10
<211> 144
<212> PRT
<213> Triticum aestivum

<400> 10
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Glu Asn Thr Asp Tyr Leu Cys Asn Met Asp Pro Tyr Ala Val Leu Lys
20 25 30
Cys Thr Ser Gln Glu Gln Lys Ser Thr Val Ala Ser Gly Lys Gly Ser
35 40 45
Asp Pro Glu Trp Asn Glu Thr Phe Val Phe Thr Val Ser Glu Asn Ala
50 55 60
Thr Glu Leu Val Ile Lys Leu Leu Asp Ser Asp Gly Gly Thr Asp Asp
65 70 75 80
Asp Ser Val Gly Glu Ala Thr Ile Pro Leu Asp Gly Val Tyr Thr Glu
85 90 95
Gly Ser Ile Pro Pro Thr Val Tyr Asn Val Val Lys Asp Glu Glu Tyr
100 105 110
Arg Gly Glu Ile Lys Ile Gly Leu Thr Phe Thr Pro Glu Glu Ala Arg
115 120 125
Asp Gln Asp Gln Pro Glu Glu Asn Tyr Gly Gly Trp Asn Gln Ser Ser
130 135 140

<210> 11
<211> 1482
<212> DNA
<213> Oryza sativa

<400> 11
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 120
 ggtgcaggaa gctgaggac acggagttct tcacgcggca ggatccctac gtctgcatcg
 180
 agtatgccac caacaagttc cgcacccgca cctgcacoga tgggggaagg aaccctactt
 240
 ttgacgagaa gtttcatata cctctcattg aggggcttcg tgagctaacc gtcacagtgt
 300
 ggaacagcaa cacgctcacc catgatgatt tcattggcaa tggcagggtg cagctgcata
 360
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 420
 ctgctgggga agtgacgctc attatgcatt ttgatgtttc agcaatgaag aacaagccgg
 480
 gaaaaatttc tgccgcgtca accacacatt ctgtttcttc agtgccggta ccagcagtac
 540
 catatgctgc cccctcacct tcatacgcac taccctctgc aggataccct gcagtaccgc
 600
 catatcaatc ctatcctgct agccatgtcc cggcgccata tcctacttca gcataccac
 660
 atccaccacc atctctgcta gctcgcgatg ttgagcatgc ggcataccct cctacaagta
 720
 caacatatcc tccacagccg taccaccac agccgcaggg acaaacatac ccaccgcagc
 780
 cgcagggaga aacataccaa ccgcagccgc agcgagaaac ataccaccgc cagcctcaag
 840
 tacaaccata cccaccaaag ccacaggac aaccataccc accgcagccg cagggacaac
 900
 catatccacc gcaaccatat ggacaaactt acccaccacc tccaaaagga cagcccacat
 960
 atccacctgc gccctatcct tcaacttacc caccagcacc atattgatat ggcacacttg
 1020
 gtggactgaa gttgtccaca taaaaagca agtaagcaac aagtgatgat cagttcttat
 1080
 atttatccag ggtatccagc cttcatcacc cagttaattg aaacaaatga aatcattcct
 1140
 gaagcgattc atgtcaacat cttagcaacc aatggtagta gttaccatct ggtatgtatc
 1200
 atatatcata gcttgcagaa tgtcacgaat ggaatttggt cgattatggt gtatgttttg
 1260
 ggcttggtgt aacagtgatc cacctttggt ctgttttgag gtcattgttg gctgttctgt
 1320
 gactgtaact actgcttttt acaaaggggg gaagcagtaa ttctagttct acctgcaact
 1380
 gcctgataag tggttaactgt gaaaagttgc agtagcttgt cgactttgta ccatgttggt
 1440
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 1482

<210> 12

<211> 308

<212> PRT

<213> Oryza sativa

<400> 12

Met Ser Ile Gln Gly Gln Ile Leu Glu Val Arg Val Thr Gly Cys Arg
 1 5 10 15

Lys Leu Arg Asp Thr Glu Phe Phe Thr Arg Gln Asp Pro Tyr Val Cys
 20 25 30

Ile Glu Tyr Ala Thr Asn Lys Phe Arg Thr Arg Thr Cys Thr Asp Gly
 35 40 45

Gly Arg Asn Pro Thr Phe Asp Glu Lys Phe His Ile Pro Leu Ile Glu

50

55

60

Gly Leu Arg Glu Leu Thr Val Thr Val Trp Asn Ser Asn Thr Leu Thr
65 70 75 80

His Asp Asp Phe Ile Gly Asn Gly Arg Val Gln Leu His Lys Val Leu
85 90 95

Thr Arg Gly Tyr Asp Asp Ala Ser Trp Pro Leu Gln Thr Arg His Met
100 105 110

Arg Ser Ala Gly Glu Val Thr Leu Ile Met His Phe Asp Val Ser Ala
115 120 125

Met Lys Asn Lys Pro Gly Lys Ile Ser Ala Ala Ser Thr Thr His Ser
130 135 140

Val Leu Pro Val Pro Val Pro Ala Val Pro Tyr Ala Ala Pro Ser Pro
145 150 155 160

Ser Tyr Ala Leu Pro Pro Ala Gly Tyr Pro Ala Val Pro Pro Tyr Gln
165 170 175

Ser Tyr Pro Ala Ser His Val Pro Ala Pro Tyr Pro Thr Ser Ala Tyr
180 185 190

Pro His Pro Pro Pro Ser Leu Leu Ala Arg Asp Val Glu His Ala Ala
195 200 205

Tyr Pro Pro Thr Ser Thr Thr Tyr Pro Pro Gln Pro Tyr Pro Pro Gln
210 215 220

Pro Gln Gly Gln Thr Tyr Pro Pro Gln Pro Gln Gly Glu Thr Tyr Gln
225 230 235 240

Pro Gln Pro Gln Arg Glu Thr Tyr Pro Pro Gln Pro Gln Val Gln Pro
245 250 255

Tyr Pro Pro Lys Pro Gln Gly Gln Pro Tyr Pro Pro Gln Pro Gln Gly
260 265 270

Gln Pro Tyr Pro Pro Gln Pro Tyr Gly Gln Thr Tyr Pro Pro Pro Pro
275 280 285

Lys Gly Gln Pro Thr Tyr Pro Pro Ala Pro Tyr Pro Ser Thr Tyr Pro
290 295 300

Pro Ala Pro Tyr
305

<210> 13

<211> 1172

<212> DNA

<213> Glycine max

<400> 13

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cttctctctt tctctgact ccatgtcgtc gataacgggc atccaggggc aacctcttga
120

ggttacggtg gtttcgtgct ccaagttgaa ggacacagaa tggatttcaa gacaagatcc
180

gtacgtttgt gttgagtatg gcagcacaaa gttccgaacc agaacctgca cagacggcgg
240

aaaaaaccog gtattccaag agaagttcat ctttccctc attgaaggcc ttcgggagct
300

caatgtcctt gtttgaaca gcaatactct caccttcgac gattttatag gaagcggaaa
 360
 gattcaattg cacaagggtc tctctcaagg cttcgatgac tctgcttggc cacttcagac
 420
 caaaactggc agatacgctg gtgaagtaaa agtcatattg cattacgcaa ttgcaaatca
 480
 aaggcataaa ttagtgtcag gccatgctcc atcagcacct ccgtatgtgg caacagcaac
 540
 tcctcccgtc ccttcttcat attctacttc ataccggcca cctccttctg ctacttccta
 600
 cccaccacca ccatcacctc cctctgcaac tccttaccat acaactggat cttattctta
 660
 cccaccggcg ccgccacctc ctacagetta ccctccctat tcctcacatt catctcccta
 720
 tccaccatca tcataccccc cacagccctc ctcgatcct cctcctcctc ccccatcato
 780
 atatccccct gcttcagctt atccatatcc accacctgca ggctatcctt ctggaatata
 840
 ccctccacca ccttactgac tgagatcttc taccttctca accaaggaac caacatcaac
 900
 atgccttgta tgccaaaagg gccttcagac tccctttcaa tgcttggtca aacgccccgt
 960
 gctttgacct tttgaggtgt cttgcttgta aagtgtttat tttatacaca ttcagatcca
 1020
 attaaagggc accatTTTTT ttttcgcaat tggatgttca ctgaccattt tccggttttc
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 1140
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
 1172

<210> 14
 <211> 258
 <212> PRT
 <213> Glycine max

<400> 14

Met	Ser	Ser	Ile	Thr	Gly	Ile	Gln	Gly	Gln	Pro	Leu	Glu	Val	Thr	Val
1				5				10					15		
Val	Ser	Cys	Ser	Lys	Leu	Lys	Asp	Thr	Glu	Trp	Ile	Ser	Arg	Gln	Asp
			20					25					30		
Pro	Tyr	Val	Cys	Val	Glu	Tyr	Gly	Ser	Thr	Lys	Phe	Arg	Thr	Arg	Thr
		35					40					45			
Cys	Thr	Asp	Gly	Gly	Lys	Asn	Pro	Val	Phe	Gln	Glu	Lys	Phe	Ile	Phe
	50					55					60				
Pro	Leu	Ile	Glu	Gly	Leu	Arg	Glu	Leu	Asn	Val	Leu	Val	Trp	Asn	Ser
	65				70					75					80
Asn	Thr	Leu	Thr	Phe	Asp	Asp	Phe	Ile	Gly	Ser	Gly	Lys	Ile	Gln	Leu
				85					90					95	
His	Lys	Val	Leu	Ser	Gln	Gly	Phe	Asp	Asp	Ser	Ala	Trp	Pro	Leu	Gln
			100					105					110		
Thr	Lys	Thr	Gly	Arg	Tyr	Ala	Gly	Glu	Val	Lys	Val	Ile	Leu	His	Tyr
		115					120					125			
Ala	Ile	Ala	Asn	Gln	Arg	His	Lys	Leu	Val	Ser	Gly	His	Ala	Pro	Ser
	130					135					140				
Ala	Pro	Pro	Tyr	Val	Ala	Thr	Ala	Thr	Pro	Pro	Val	Pro	Ser	Ser	Tyr
145					150					155					160

Ser Thr Ser Tyr Pro Pro Pro Pro Ser Ala Thr Ser Tyr Pro Pro Pro
165 170 175

Pro Ser Pro Pro Ser Ala Thr Pro Tyr His Thr Thr Gly Ser Tyr Ser
180 185 190

Tyr Pro Pro Pro Pro Pro Pro Pro Thr Ala Tyr Pro Pro Tyr Ser Ser
195 200 205

His Ser Ser Pro Tyr Pro Pro Ser Ser Tyr Pro Pro Gln Pro Ser Ser
210 215 220

Tyr Pro Pro Pro Pro Pro Pro Ser Ser Tyr Pro Pro Ala Ser Ala Tyr
225 230 235 240

Pro Tyr Pro Pro Pro Ala Gly Tyr Pro Ser Gly Ile Tyr Pro Pro Pro
245 250 255

Pro Tyr

<210> 15
<211> 757
<212> DNA
<213> Zea mays

<400> 15
accacgcgt cgcgccacgc gtcgcgcgcg ccgcgcgaag agaggagaga ggcctccaa 60
cgccacctgg aggagaggac agcgcgccag ggagggggag gaggaagaag aacatgggga 120
agggcgctcct gaaggtgcac ctgcgtcgacg ccaaggggct ctccggcaac gatttcttag 180
ggaagctgga cccctacgtg atcatgcagt accggagcca ggagcgcaag agcagcgctcg 240
cccgagacca aggaaggaac ccgtgctgga acgaggtgtt caagttccag atcaactcgg 300
ccgcggccaa cgtgcagcac aagctcatcc tccggatcat ggaccacgac aacttctcca 360
gcgacgactt cctcggcgag gcgacgatcg acgtgacgga catcgtcagc ctgggcgcgcg 420
agcgcggcac gtaccacctc aacgcggcca agcacaacgt ggtcctcgcc gacaagacgt 480
accacggcga gatcaaggtc gccatcacct tcacctccac ccagaccag gttcaggaag 540
atggaggagc aattggagga tggaggcaca gtagctttta tcagtgaag tgataggcgt 600
cgtggactct ctcaagttct ttggttgctt ggtggtggtt cgggttggtat gtagtttttg 660
tttatgtcca cgagcaatct gtgcctaaca tttctagggt tcaattcaat gattcaatcc 720
aaccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaag 757

<210> 16
<211> 157
<212> PRT
<213> Zea mays

<400> 16
Met Gly Lys Gly Val Leu Lys Val His Leu Val Asp Ala Lys Gly Leu
1 5 10 15

Ser Gly Asn Asp Phe Leu Gly Lys Leu Asp Pro Tyr Val Ile Met Gln
20 25 30

Tyr Arg Ser Gln Glu Arg Lys Ser Ser Val Ala Arg Asp Gln Gly Arg
35 40 45

Asn Pro Cys Trp Asn Glu Val Phe Lys Phe Gln Ile Asn Ser Ala Ala
50 55 60

Ala Asn Val Gln His Lys Leu Ile Leu Arg Ile Met Asp His Asp Asn
65 70 75 80

Phe Ser Ser Asp Asp Phe Leu Gly Glu Ala Thr Ile Asp Val Thr Asp
85 90 95

Ile Val Ser Leu Gly Ala Glu Arg Gly Thr Tyr His Leu Asn Ala Ala
100 105 110
Lys His Asn Val Val Leu Ala Asp Lys Thr Tyr His Gly Glu Ile Lys
115 120 125
Val Ala Ile Thr Phe Thr Ser Thr Gln Thr Gln Val Gln Glu Asp Gly
130 135 140
Gly Ala Ile Gly Gly Trp Arg His Ser Ser Phe Asn Gln
145 150 155

<210> 17
<211> 422
<212> DNA
<213> Hevea brasiliensis

<220>
<221> unsure
<222> (410)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (415)
<223> n = A, C, G or T

<400> 17
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ctgggctatt ggaagtgcag ctggtgaatg caaaaggcct cagaggcact gatttcttag 180
gtaagattga tccatatgtt atcgtgaagt acaaaaaacca agagcgcgag agcagtgtcg 240
ccagaggtca aggtgggaat ccagtgtgga atgagaaact cacattcaag gtggaatc 300
cagggcaagg tgaagagtac aagctcattt taaaaatcat ggacaaggac accttctctg 360
ctgatgattt gcttgggcca tgctacgata tatgtgaagg atttggtggn attangaatg 420
ga 422

<210> 18
<211> 102
<212> PRT
<213> Hevea brasiliensis

<220>
<221> UNSURE
<222> (99)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (101)
<223> Xaa = any amino acid

<400> 18
Met Ala Thr Gly Leu Leu Glu Val Gln Leu Val Asn Ala Lys Gly Leu
1 5 10 15
Arg Gly Thr Asp Phe Leu Gly Lys Ile Asp Pro Tyr Val Ile Val Lys
20 25 30
Tyr Lys Asn Gln Glu Arg Glu Ser Ser Val Ala Arg Gly Gln Gly Gly
35 40 45
Asn Pro Val Trp Asn Glu Lys Leu Thr Phe Lys Val Glu Tyr Pro Gly
50 55 60
Gln Gly Glu Glu Tyr Lys Leu Ile Leu Lys Ile Met Asp Lys Asp Thr

65

70

75

80

Phe Ser Ala Asp Asp Leu Leu Gly His Ala Thr Ile Tyr Val Lys Asp
85 90 95

Leu Leu Xaa Leu Xaa Met
100

<210> 19

<211> 486

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (430)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (464)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (486)

<223> n = A, C, G or T

<400> 19

agaagaatag	aatcttcaga	gacatggcaa	ttgggttcat	ggaggtgcag	cttgtgaaag	60
caaaaggcct	gcgagacact	gatatctttg	gtaaaatgga	tccctatggt	ctgatacaat	120
acaaaggcca	agagaagagg	agtgggtgctg	ctaattggcaa	aggcaaaaat	ccggtatgga	180
atgagaaaatt	tatcttcaaa	gtagaatatc	ctggatcaag	caatcaacac	aagctcatcc	240
tcaaaattat	ggataaagac	ttatatacag	acgacttcgt	cggagaagca	ataatccatg	300
taggggattt	attggcccaa	ggagtagaga	acggaggagc	caaattacag	actctcaagt	360
atagagtggg	tcgtgctaac	aagtcttatt	gtggtgaaat	tgatgttggg	tgttactttt	420
accccgaaan	gtgggaagac	aaatthttgtg	ggaagaagac	atangaggat	ggaaaagaaa	480
gtgacn						486

<210> 20

<211> 154

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (136)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (147)

<223> Xaa = any amino acid

<400> 20

Met	Ala	Ile	Gly	Phe	Met	Glu	Val	Gln	Leu	Val	Lys	Ala	Lys	Gly	Leu
1				5					10					15	

Arg	Asp	Thr	Asp	Ile	Phe	Gly	Lys	Met	Asp	Pro	Tyr	Val	Leu	Ile	Gln
			20					25					30		

Tyr	Lys	Gly	Gln	Glu	Lys	Arg	Ser	Gly	Val	Ala	Asn	Gly	Lys	Gly	Lys
		35					40					45			

Asn	Pro	Val	Trp	Asn	Glu	Lys	Phe	Ile	Phe	Lys	Val	Glu	Tyr	Pro	Gly
	50					55						60			

Ser Ser Asn Gln His Lys Leu Ile Leu Lys Ile Met Asp Lys Asp Leu
65 70 75 80

Tyr Thr Asp Asp Phe Val Gly Glu Ala Ile Ile His Val Gly Asp Leu
85 90 95

Leu Ala Gln Gly Val Glu Asn Gly Gly Ala Lys Leu Gln Thr Leu Lys
100 105 110

Tyr Arg Val Val Arg Ala Asn Lys Ser Tyr Cys Gly Glu Ile Asp Val
115 120 125

Gly Cys Tyr Phe Tyr Pro Glu Xaa Trp Glu Asp Lys Phe Cys Gly Lys
130 135 140

Lys Thr Xaa Glu Asp Gly Lys Glu Ser Asp
145 150

<210> 21

<211> 862

<212> DNA

<213> Glycine max

<400> 21

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cggttagagt	gagaaagaga	tggaattgg	gttcatggag	gtgcagcttg	tgaaagcaaa	120
ggagttgtgt	gacactgatt	tctttggtag	tatggacccg	tatgttggtga	tacaatacaa	180
cggccaagag	caaaggagta	gtgttgctaa	gggacagggc	aataatccgg	tatggaatga	240
gaaatttggtg	ttcaaggtag	aatatcctac	actgagtaat	tcatacaaga	ttatcttaaa	300
aatcatggac	aaggatcttt	tatctgcaga	tgactttggt	ggtcaagcca	tagtctatgt	360
ggaagattta	ttagccatag	gggtagagga	tggtgcggt	gagctacaac	ctctaaagta	420
cagagtaatt	cgtgcagatc	aatcttattg	tgagagaaatt	gatcttggtga	taacttttaa	480
ggtggaagaa	gagttcaatg	gagaagctaa	acgaggatcg	aaggacagta	aatagtattt	540
gcaatagcag	ttggccaaca	tgaatatcaa	ttgatttcaa	tgagatgttt	ggaatcatca	600
tcatgtagt	agtttcatct	ttttagttgt	atatgatcct	tttggaaagt	aggatcaatg	660
catagataaa	tttactaaat	tttatgccat	caaattagta	atagtatgca	ttattaatct	720
tctaatttat	cttcaccata	attaatctca	ttgatgattc	aatcttgtag	ttccttaaca	780
tctatatact	atatgggttt	gaacctttta	aaaaaaagaa	aaaaaaaaaa	aaaaaaaaaa	840
aaaaaaaaaa	aaaaaaaaaa	aa				862

<210> 22

<211> 151

<212> PRT

<213> Glycine max

<400> 22

Met Ala Ile Gly Phe Met Glu Val Gln Leu Val Lys Ala Lys Glu Leu
1 5 10 15

Cys Asp Thr Asp Phe Phe Gly Ser Met Asp Pro Tyr Val Val Ile Gln
20 25 30

Tyr Asn Gly Gln Glu Gln Arg Ser Ser Val Ala Lys Gly Gln Gly Asn
35 40 45

Asn Pro Val Trp Asn Glu Lys Phe Val Phe Lys Val Glu Tyr Pro Thr
50 55 60

Leu Ser Asn Ser Tyr Lys Ile Ile Leu Lys Ile Met Asp Lys Asp Leu
65 70 75 80

Leu Ser Ala Asp Asp Phe Val Gly Gln Ala Ile Val Tyr Val Glu Asp
85 90 95

Leu Leu Ala Ile Gly Val Glu Asp Gly Ala Ala Glu Leu Gln Pro Leu

100

105

110

Lys Tyr Arg Val Ile Arg Ala Asp Gln Ser Tyr Cys Gly Glu Ile Asp
115 120 125

Leu Gly Ile Thr Phe Lys Val Glu Glu Glu Phe Asn Gly Glu Ala Lys
130 135 140

Arg Gly Ser Lys Asp Ser Lys
145 150

<210> 23

<211> 860

<212> DNA

<213> Triticum aestivum

<400> 23

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gtcacaaggc aaaggacaga ggaggtgctt gttcaggtct cctgctagat ccggaggcga 120
tgggcagggg cgtgctggag gtgcatctcg tcgacgcca gggcctcttc ggcagcgatt 180
tcctagggaa gatcgacccg tatgtaatcg tgcaataccg gagccaggag cgcaagagca 240
gcacctccag agatgagggg aggaaccgga gctggaacga ggtgttccg ttccagatca 300
actcctctgc ggccaacggg cagcacaagc tcttctccg gatcatggac cagcacaact 360
tctccagcga cgacttctc ggccaagcga cgatcaacgt gaccgatctg atcagcaccg 420
gcatggagag cggcgctcg cagctgaacg cggcaaagta cagcgttggt tccgctgata 480
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acggagggca ggtcggaggc tggacgcaca gctctcgca gtagagcatg taacgtcctt 600
gcccttcgct cgtagcttta gtgttgatg ctatgatgtc cgtgactgaa tgatgtgatt 660
ccaagtgtat gtacgttgca cctgtagtag ctttttagaa gatgtatatg tactagtagc 720
cagaagtcag aactcgtagc aggctagagg cgtcaattcc gttaattaat tgtcgatttg 780
tggttcttat tttaggggga attgtgattc tggatgcgaa caccaaaaaa aaaaaaaaaa 840
aaaaaaaaa aaaaaaaaaa
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<210> 24

<211> 154

<212> PRT

<213> Triticum aestivum

<400> 24

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Met Gly Arg Gly Val Leu Glu Val His Leu Val Asp Ala Lys Gly Leu
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Phe Gly Ser Asp Phe Leu Gly Lys Ile Asp Pro Tyr Val Ile Val Gln
 20 25 30
Tyr Arg Ser Gln Glu Arg Lys Ser Thr Ser Arg Asp Glu Gly Arg
 35 40 45
Asn Pro Ser Trp Asn Glu Val Phe Arg Phe Gln Ile Asn Ser Ser Ala
 50 55 60
Ala Asn Gly Gln His Lys Leu Phe Leu Arg Ile Met Asp His Asp Asn
 65 70 75 80
Phe Ser Ser Asp Asp Phe Leu Gly Gln Ala Thr Ile Asn Val Thr Asp
 85 90 95
Leu Ile Ser Thr Gly Met Glu Ser Gly Ala Ser Gln Leu Asn Ala Ala
100 105 110
Lys Tyr Ser Val Val Ser Ala Asp Asn Ser Tyr His Gly Glu Ile Arg
115 120 125
Val Gly Leu Thr Phe Thr Ala Thr Lys Val Glu Glu Asp Gly Gly Gln
130 135 140
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Val Gly Gly Trp Thr His Ser Ser Arg Glu
145 150

<210> 25
<211> 914
<212> DNA
<213> Oryza sativa

<400> 25
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gaagccaagt ttgcgcatta catcaaaggg ttcttttgat gcgaccaatg ctgtgaagag 120
tgtaactagc agtatctcta gcgcttcagg gaagcatgtc gctgacgata caagagaatt 180
tgttggagag ctgaacatta cagtggtaag aggtattcag ttggccgtca gagacatgct 240
aacgagcgat ccataatgtt ttctaacact tggggagcag aaagctcaaa ccactgttaa 300
accgagtgcac ttgaaccag tatggaatga ggtgcttaag atatcaattc ctcgaaatta 360
tggacctctt aaacttgaag tatacgacca tgatacgttc tctgctgatg atatcatggg 420
ggaagcggag atagatcttc aaccaatgat cacagccgtc atggccttg gagatccctc 480
gcggtgttgg gacatgcaaa ttggaaggtg gttcatgacc aaagacaatg ccctggtgaa 540
agatagcact gtcaatgttg tgcgggcaa ggtaaaacag gaagtgcacc taaagttgca 600
gaatgtagaa tcaggtgaga tggagttaga actggaatgg gttccaatac cctagattaa 660
taaagctcga ttggttctct gccaaaaaaa attactcaag aagcgtcagt tttgtaattt 720
aaatgaatgg cttcaaattc cgtgtactta ctgaatctct gtcttcaaca tttggccac 780
ccgaacgaaa ttcgtaaaaa tgccattgta aaatatcatg ttgtaatccg tcggctgcac 840
tcacgaccaa ttatattatt ctttagtgaa gtgtgctttc aaccctgtgt cataaaaaaa 900
aaaaaaaaaa aaaa 914

<210> 26
<211> 217
<212> PRT
<213> Oryza sativa

<400> 26
Phe Trp Lys Lys Arg Ser Pro Lys Thr Leu Tyr Ser Ile Val Glu Thr
1 5 10 15
Gln Asp Phe Leu Lys Pro Ser Leu Arg Ile Thr Ser Lys Gly Ser Phe
20 25 30
Asp Ala Thr Asn Ala Val Lys Ser Val Thr Ser Ser Ile Ser Ser Ala
35 40 45
Ser Gly Lys His Val Ala Asp Asp Thr Arg Glu Phe Val Gly Glu Leu
50 55 60
Asn Ile Thr Val Val Arg Gly Ile Gln Leu Ala Val Arg Asp Met Leu
65 70 75 80
Thr Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Glu Gln Lys Ala Gln
85 90 95
Thr Thr Val Lys Pro Ser Asp Leu Asn Pro Val Trp Asn Glu Val Leu
100 105 110
Lys Ile Ser Ile Pro Arg Asn Tyr Gly Pro Leu Lys Leu Glu Val Tyr
115 120 125
Asp His Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Glu Ile
130 135 140
Asp Leu Gln Pro Met Ile Thr Ala Val Met Ala Phe Gly Asp Pro Ser
145 150 155 160
Arg Val Gly Asp Met Gln Ile Gly Arg Trp Phe Met Thr Lys Asp Asn
165 170 175
Ala Leu Val Lys Asp Ser Thr Val Asn Val Val Ser Gly Lys Val Lys

180

185

190

Gln Glu Val His Leu Lys Leu Gln Asn Val Glu Ser Gly Glu Met Glu
195 200 205

Leu Glu Leu Glu Trp Val Pro Ile Pro
210 215

<210> 27

<211> 770

<212> DNA

<213> *Oryza sativa*

<400> 27

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aggtcctcct cgtctgcgcc aagggcctcg aggacactga cttcttgaac gacatggacc 180
cctacgtgat cctcacctgc cgcactcagg agcagaaaag cagcgttgca aaaggagcag 240
gaagcgagcc tgaatggaac gagaccttcg tcttcaccgt ctccgacgat gttccacagc 300
tcaatgtcaa gatcatggac agtgatecct totcagctga cgatttcgtc ggtgaagcaa 360
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tgctgtctac taatgagcat caacgagagg agatcttgct tcaagaatta atgtgcttgt 600
caacaatact ccgtgctatg atgtcctaag aactgaaaca tccatttata tgtatatccc 660
agaccattga cttgctctgc ctaaattttg tatatTTTTT actacaaaga tgtgatggtg 720
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<210> 28

<211> 145

<212> PRT

<213> *Oryza sativa*

<400> 28

Met Val His Gly Lys Leu Glu Val Leu Leu Val Cys Ala Lys Gly Leu
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Glu Asp Thr Asp Phe Leu Asn Asp Met Asp Pro Tyr Val Ile Leu Thr
20 25 30

Cys Arg Thr Gln Glu Gln Lys Ser Ser Val Ala Lys Gly Ala Gly Ser
35 40 45

Glu Pro Glu Trp Asn Glu Thr Phe Val Phe Thr Val Ser Asp Asp Val
50 55 60

Pro Gln Leu Asn Val Lys Ile Met Asp Ser Asp Ala Phe Ser Ala Asp
65 70 75 80

Asp Phe Val Gly Glu Ala Asn Ile Pro Leu Glu Pro Val Phe Leu Glu
85 90 95

Gly Ser Leu Pro Pro Ala Val His Arg Val Val Lys Glu Glu Lys Tyr
100 105 110

Cys Gly Glu Ile Lys Val Ala Leu Thr Phe Thr Pro Ala Ala Glu Thr
115 120 125

Arg His His His Asn His Glu Asn Glu Gly Glu Gly Tyr Ser Ser Trp
130 135 140

Asn

145

<210> 29

<211> 958

<212> DNA
<213> Glycine max

<400> 29
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aagcatattc ctgagtcaaa tagttctgtc catatagaat ttgtgaagtg agagtccaac 180
ctttcatttt caattttcaa agatgcctcg tggaacactt gaagttgttc tgatcagcgc 240
caaaggaatc gatgacaatg attttctctc cagcatagat ccttatgtga ttctcacata 300
cagggcacag gagaaaaaga gcaactgtgca agaagatgct ggatccaagc cacaatggaa 360
tgagagcttt cttttcactg tctctgacag tgcttctgaa cttaatctga agataatgga 420
taaagacaac tttagtcaag atgattgtct tggcgaggga accattcatt tagatccagt 480
gtttgaagcc ggtagcattc cagaaaactgc ttacaagggt gtgaaggacg aagaatattg 540
tggtgagatt aagggtggctc tcactttcac tgctgagaga aatgaggagc agggttatga 600
tgacacctgaa gagagctatg gtggatggaa agaatccagt ggggaatatt aaagtgaag 660
aagaatttac atacttcaat ggccagactt acctttataa tgaaaaataa gcagtttttg 720
tgtcactctt aggcaatttc cattattgtg ttttctggtg tgaagatcca atagtgttgt 780
gcttttaggt tgcattcctc cctttggata ttaaagtaca ttatgcttga tatattatct 840
tttatgcac agttaaacat tagaagagca gtgctatttt atttaaaaaa aaaaaaaaaa 900
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 958

<210> 30
<211> 149
<212> PRT
<213> Glycine max

<400> 30
Met Pro Arg Gly Thr Leu Glu Val Val Leu Ile Ser Ala Lys Gly Ile
1 5 10 15
Asp Asp Asn Asp Phe Leu Ser Ser Ile Asp Pro Tyr Val Ile Leu Thr
20 25 30
Tyr Arg Ala Gln Glu Lys Lys Ser Thr Val Gln Glu Asp Ala Gly Ser
35 40 45
Lys Pro Gln Trp Asn Glu Ser Phe Leu Phe Thr Val Ser Asp Ser Ala
50 55 60
Ser Glu Leu Asn Leu Lys Ile Met Asp Lys Asp Asn Phe Ser Gln Asp
65 70 75 80
Asp Cys Leu Gly Glu Ala Thr Ile His Leu Asp Pro Val Phe Glu Ala
85 90 95
Gly Ser Ile Pro Glu Thr Ala Tyr Lys Val Val Lys Asp Glu Glu Tyr
100 105 110
Cys Gly Glu Ile Lys Val Ala Leu Thr Phe Thr Ala Glu Arg Asn Glu
115 120 125
Glu Gln Gly Tyr Asp Ala Pro Glu Glu Ser Tyr Gly Gly Trp Lys Glu
130 135 140
Ser Ser Gly Glu Tyr
145

<210> 31
<211> 695
<212> DNA
<213> Triticum aestivum

<400> 31
gcacgaggag agatccaaga ctaggcgggc cggccggagg agatcgagaa ggaggaggag 60
acatggtgcg cgggaagctg gaggtgctgc tcgtctccgc caagggcctc gacgactccg 120
atttcttcaa tagcatggac ccgtacgtga tcctcacctg ccgcagccac gagcagaaga 180

gcaccgtcgc atcaggagca gggagcgcgc ctgagtggaa cgagaccttc gtcttcgccg 240
tctccggcga cgctccggag ctcaggggtca agatcatgga cagcgacgcc ctctcgcccg 300
acgacctcgt cggagaagca tgtatccgcg tggaggctgt gctccaggag ggcagcctgc 360
cgccggccgt gcaccgggtc gtcaaggacg aggagtaccg cggggagatc aagatcgcg 420
tcaccttcac cccggcagag gaaaacgagg aggaggagga gagctacggc ggctggaatc 480
agtccacctg aaaaaggcca gcgagccagc aagatgggtg tgtatgtctg actgtcataa 540
tggatagaaa ggctttggat atccttgatg tgtgtgacag acagggcatt caggaaaacg 600
agtaaaaata ggggaaatat gtatcgatgc atgcatgaag tactaatcaa gcaattcacc 660
gcatcgtttt gtattgcaaa aaaaaaaaaa aaaaa 695

<210> 32
<211> 142
<212> PRT
<213> Triticum aestivum

<400> 32
Met Val Arg Gly Lys Leu Glu Val Leu Leu Val Ser Ala Lys Gly Leu
1 5 10 15
Asp Asp Ser Asp Phe Phe Asn Ser Met Asp Pro Tyr Val Ile Leu Thr
20 25 30
Cys Arg Ser His Glu Gln Lys Ser Thr Val Ala Ser Gly Ala Gly Ser
35 40 45
Glu Pro Glu Trp Asn Glu Thr Phe Val Phe Ala Val Ser Gly Asp Ala
50 55 60
Pro Glu Leu Arg Val Lys Ile Met Asp Ser Asp Ala Leu Ser Ala Asp
65 70 75 80
Asp Leu Val Gly Glu Ala Cys Ile Pro Leu Glu Ala Val Leu Gln Glu
85 90 95
Gly Ser Leu Pro Pro Ala Val His Arg Val Val Lys Asp Glu Glu Tyr
100 105 110
Arg Gly Glu Ile Lys Ile Ala Leu Thr Phe Thr Pro Ala Glu Glu Asn
115 120 125
Glu Glu Glu Glu Glu Ser Tyr Gly Gly Trp Asn Gln Ser Thr
130 135 140

<210> 33
<211> 617
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (421)
<223> n = A, C, G or T

<400> 33
cacgccgcct ccatgtgggt ggggaggcaa acgcgttcgt ccatctctga aactcaaacg 60
ccttgatttg gagcatacta caggagtact tctgtacaaa tataaatacc cctggcgagt 120
tgggttggtt ctatctcgca atcgaggcgt tttttttctg ctctgtaagt tcgtggctga 180
tccagcgagc gagcgagcag accggcggcc aaccgcggag ggagagatgg cgcaggggac 240
gctggagggtg cttctcgctg gagccagggg cctcgagAAC accgattacc tgagcaacat 300
ggaccocctac gcgcttctgc aatgtcgctc ccacgagcag aagagcagcg tcgcatctgg 360
caaaggctgt gaacctgagt ggaacgagac cttcgtgttc accgtctcca acggcgcaca 420
ngagctgttc atcaagctcc tggacagtga cgggtggcact gatgacgatt ttgttggtga 480
agcaacgatt cctctggaag ccagttttaca cggaaggaa gcatctcttc cgactgttta 540
caatgtttgt aaagacgaag aataccgcgg agaaatcaaa gttggcctca cgttcactcc 600
agaggtaaac catctca 617

<210> 34
<211> 202
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (140)
<223> Xaa = any amino acid

<400> 34
Thr Pro Pro Pro Cys Gly Trp Gly Gly Lys Arg Val Arg Pro Ser Leu
1 5 10 15
Lys Leu Lys Arg Leu Val Leu Glu His Thr Thr Gly Val Leu Leu Tyr
20 25 30
Lys Tyr Lys Tyr Pro Trp Arg Val Gly Leu Gly Leu Ser Arg Asn Arg
35 40 45
Gly Val Phe Phe Leu Leu Arg Lys Phe Val Val Asp Pro Ala Ser Glu
50 55 60
Arg Ala Asp Arg Arg Pro Thr Ala Glu Gly Glu Met Ala Gln Gly Thr
65 70 75 80
Leu Glu Val Leu Leu Val Gly Ala Arg Gly Leu Glu Asn Thr Asp Tyr
85 90 95
Leu Ser Asn Met Asp Pro Tyr Ala Leu Leu Gln Cys Arg Ser His Glu
100 105 110
Gln Lys Ser Ser Val Ala Ser Gly Lys Gly Cys Glu Pro Glu Trp Asn
115 120 125
Glu Thr Phe Val Phe Thr Val Ser Asn Gly Ala Xaa Glu Leu Phe Ile
130 135 140
Lys Leu Leu Asp Ser Asp Gly Gly Thr Asp Asp Asp Phe Val Gly Glu
145 150 155 160
Ala Thr Ile Pro Leu Glu Ala Ser Leu His Gly Lys Glu Ala Phe Leu
165 170 175
Pro Thr Val Tyr Asn Val Val Lys Asp Glu Glu Tyr Arg Gly Glu Ile
180 185 190
Lys Val Gly Leu Thr Phe Thr Pro Glu Val
195 200

<210> 35
<211> 544
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (415)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (478)
<223> n = A, C, G or T

<220>

<221> unsure
 <222> (494)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (509)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (515)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (531)..(532)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (542)
 <223> n = A, C, G or T

<400> 35
 gttcgttcac gccacaggca aggcacaggg gcttgtgagg gagagcgagg agcggaggag 60
 gacatgggtgc acgggacgct ggaagtgctg ctctgttgggg ccaagggcct cgagaacacc 120
 gattacctct gtaacatgga tccgtatgca attctcaagt gccgttcaca ggagcagaag 180
 agcagtattg caactggaaa aggaactacc cctgagtggga atgaaaactt tatcttcact 240
 gtgtctgacc ggacaacaga cttggtaatc aagcttatgg acagtgatac aggcacagca 300
 gatgactttg ttggtgaagc aacgattoca ttggaagcag tgtatactga aaggagcatt 360
 ccaccaacac tctataatgt tgtgaaaggt gaaaaatact gcgggggaaat caaantggtc 420
 tcacattcac tcctgaggat actcgcaagc ggggtctccaa aggacttcgt ggtggaanca 480
 tcattcttaag ctantcttta gggtcacana cacancacaa tcatcgcttg nncctcaccg 540
 tnat 544

<210> 36
 <211> 130
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (118)
 <223> Xaa = any amino acid

<400> 36
 Met Val His Gly Thr Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu
 1 5 10 15
 Glu Asn Thr Asp Tyr Leu Cys Asn Met Asp Pro Tyr Ala Ile Leu Lys
 20 25 30
 Cys Arg Ser Gln Glu Gln Lys Ser Ser Ile Ala Thr Gly Lys Gly Thr
 35 40 45
 Thr Pro Glu Trp Asn Glu Asn Phe Ile Phe Thr Val Ser Asp Arg Thr
 50 55 60
 Thr Asp Leu Val Ile Lys Leu Met Asp Ser Asp Thr Gly Thr Ala Asp
 65 70 75 80
 Asp Phe Val Gly Glu Ala Thr Ile Pro Leu Glu Ala Val Tyr Thr Glu
 85 90 95
 Arg Ser Ile Pro Pro Thr Leu Tyr Asn Val Val Lys Gly Glu Lys Tyr

100

105

110

Cys Gly Glu Ile Lys Xaa Gly Leu Thr Phe Thr Pro Glu Asp Thr Arg
 115 120 125

Lys Arg
 130

<210> 37
 <211> 459
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (435)
 <223> n = A, C, G or T

<400> 37
 gccgagcttt ccattttttca actcctagtc ctatacatatc agcgggaaccc cggggctcgg 60
 atcggatcta cagcaattag tctcgacctt cagtcgtgcc gcctgctcat cagcatataa 120
 ttctgatcgc agcgagcggg agaggaaggc gagatcaggc cgggagagaa gatggcgag 180
 gggacgctgg aggtgctgct cgtgggagcc aagggcctcg agaaccacca ctacctctgc 240
 aacatggacc cgtacgcggt tctaaaatgc acctcgcagg agcaaaaagag caccgtcgcc 300
 tctggaaagg gaagtgatcc tgagtggaaac gaaacctttg tgttcaccgt ctctgagaat 360
 gcaactgagc ttgtcatcaa gctactggac agtgatggtg gcacggacga cgacagcggt 420
 ggtgaagcaa cgatncattg gatggagtgt acactgaag 459

<210> 38
 <211> 87
 <212> PRT
 <213> Triticum aestivum

<400> 38
 Met Ala Gln Gly Thr Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu
 1 5 10 15
 Glu Asn Thr Asp Tyr Leu Cys Asn Met Asp Pro Tyr Ala Val Leu Lys
 20 25 30
 Cys Thr Ser Gln Glu Gln Lys Ser Thr Val Ala Ser Gly Lys Gly Ser
 35 40 45
 Asp Pro Glu Trp Asn Glu Thr Phe Val Phe Thr Val Ser Glu Asn Ala
 50 55 60
 Thr Glu Leu Val Ile Lys Leu Leu Asp Ser Asp Gly Gly Thr Asp Asp
 65 70 75 80
 Asp Ser Val Gly Glu Ala Thr
 85

<210> 39
 <211> 417
 <212> DNA
 <213> Oryza sativa

<400> 39
 atcgtaacct cagctcctct ctttcttccc ctcccccgct cctccgcgag acgacccgcg 60
 cccgtagcca tccatgtcga tacaaggcca gatcctcgaa gtcagagtca ctgggtgcag 120
 gaagctgagg gacacggagt tcttcacgcg gcaggatccc tacgtctgca tcgagtatgc 180
 caccaacaag ttccgcaccc gcacctgcac cgatggggga aggaacccta cttttgacga 240
 gaagtttcat atacctctca ttgaggggct tcgtgagcta accgtcacag tgtggaacag 300
 caacacgctc acccatgatg atttcattgg caatggcagg gtgcaagctg cataaggtgc 360
 ttacgcgctg ctatgatgat gcctcaaggg ccctccagac acgccatatg aggtctg 417

<210> 40
<211> 83
<212> PRT
<213> Oryza sativa

<400> 40
Leu Glu Val Arg Val Thr Gly Cys Arg Lys Leu Arg Asp Thr Glu Phe
1 5 10 15
Phe Thr Arg Gln Asp Pro Tyr Val Cys Ile Glu Tyr Ala Thr Asn Lys
20 25 30
Phe Arg Thr Arg Thr Cys Thr Asp Gly Gly Arg Asn Pro Thr Phe Asp
35 40 45
Glu Lys Phe His Ile Pro Leu Ile Glu Gly Leu Arg Glu Leu Thr Val
50 55 60
Thr Val Trp Asn Ser Asn Thr Leu Thr His Asp Asp Phe Ile Gly Asn
65 70 75 80

Gly Arg Val

<210> 41
<211> 550
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (534)
<223> n = A, C, G or T

<400> 41
ggtgaattgc aatttcaatt aattagaatt caacgtttgc aaattgcata ttgttcttct 60
cttcctctct tcctctgact ccatgtcgtc gataacgggc atccagggcc aacctcttga 120
ggttacgggtg gtttcgtgct ccaagttgaa ggacacagaa tggatttcaa ggcaagatcc 180
gtacgtttgt gttgagtatg gcagcacaaa gttccgaacc agaacctgca cagacggcgg 240
aaaaaatccg gtattccaag agaagttcat cttccccctc attgaaggcc ttcgggagct 300
caatgtcctt gtttgaaca gcaatactct caccttggac gattttatag gaagcggaaa 360
gattcaattg cacaaggttc tctctcaagg cttcgatgac tctgcttggc cacttcagac 420
caaaactggc agatacgtg gtgaagtcaa agtcatattg cattacgcaa ttgcaaataca 480
tcaaaggcat aatcagtggt caagccatgc tccatcaaca cctccgtatg tggnaacaac 540
aactcctccc 550

<210> 42
<211> 116
<212> PRT
<213> Glycine max

<400> 42
Met Ser Ser Ile Thr Gly Ile Gln Gly Gln Pro Leu Glu Val Thr Val
1 5 10 15
Val Ser Cys Ser Lys Leu Lys Asp Thr Glu Trp Ile Ser Arg Gln Asp
20 25 30
Pro Tyr Val Cys Val Glu Tyr Gly Ser Thr Lys Phe Arg Thr Arg Thr
35 40 45
Cys Thr Asp Gly Gly Lys Asn Pro Val Phe Gln Glu Lys Phe Ile Phe
50 55 60
Pro Leu Ile Glu Gly Leu Arg Glu Leu Asn Val Leu Val Trp Asn Ser
65 70 75 80

Asn Thr Leu Thr Leu Asp Asp Phe Ile Gly Ser Gly Lys Ile Gln Leu
85 90 95

His Lys Val Leu Ser Gln Gly Phe Asp Asp Ser Ala Trp Pro Leu Gln
100 105 110

Thr Lys Thr Gly
115

<210> 43
<211> 424
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (169)..(170)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (172)..(173)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (178)..(179)..(180)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (183)
<223> n = A, C, G or T

<400> 43
accacacgct ccgccacgc gtccgcgcgc ccgcgcgaag agaggagaga gcgcctccaa 60
cgccacctgg aggagaggac agcgcgccag ggagggggag gaggaagaag aacatgggga 120
agggcgctct gaaggtgcac ctcgctcgac ccaaggggct ctccggcann gnnttctnnn 180
ggnagctgga cccctacgtg atcatgcagt accggagcca ggagcgcaag agcagcgctcg 240
cccgagacca aggaaggaac ccgtgctgga acgaggtgtt caagttccag atcaactcgg 300
ccgcggccaa cgtgcagcac aagctcatcc tccggatcat ggaccacgac aacttctcca 360
gcgacgactt ctccggcgagg cgacgatcga cgtgacggac atcgtcagcc tgggcgcgga 420
gcgc 424

<210> 44
<211> 85
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (18)..(19)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (21)..(22)..(23)
<223> Xaa = any amino acid

<400> 44
Gly Lys Gly Val Leu Lys Val His Leu Val Asp Ala Lys Gly Leu Ser
1 5 10 15

Gly Xaa Xaa Phe Xaa Xaa Xaa Leu Asp Pro Tyr Val Ile Met Gln Tyr
20 25 30

Arg Ser Gln Glu Arg Lys Ser Ser Val Ala Arg Asp Gln Gly Arg Asn
35 40 45

Pro Cys Trp Asn Glu Val Phe Lys Phe Gln Ile Asn Ser Ala Ala Ala
50 55 60

Asn Val Gln His Lys Leu Ile Leu Arg Ile Met Asp His Asp Asn Phe
65 70 75 80

Ser Ser Asp Asp Phe
85

<210> 45
<211> 548
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (291)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (349)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (417)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (437)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (446)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (486)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (492)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (506)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (525)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (528)
<223> n = A, C, G or T

<220>
 <221> unsure
 <222> (544)
 <223> n = A, C, G or T

<400> 45
 ttaaattgta agaattttgc tgacttgtaa gtttcagaga cgaagacaca cggtttagagt 60
 gagaaagaga tggcaattgg gttcatggag gtgcagcttg tgaaagcaaa ggagttgtgt 120
 gacactgatt tctttggttag tatggaccog tatgttggtga tacaatacaa cggccaagag 180
 caaaggagta gtgttgctaa gggacagggc aataatccgg tatggaatga gaaatttgtg 240
 ttcaaggtag aatatacctac actgagtaat tcatacaaga ttatcttaaa natcatggac 300
 aaggatcttt tatctgcaga tgactttggt ggccaagcca tagtcctang tgggaagatt 360
 tattagccat aaggggtaga ggatgggtgcc ggctgagcta caacctccta aagtacnaga 420
 gtaattccgt gcagatnaat ccttantggt ggagaaattg atcttgggat aactttttaa 480
 ggggnaaga angagttcaa tggagnaagc ctaaaccaag gatchnaang acagtaaatt 540
 agtntttc 548

<210> 46
 <211> 89
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (71)
 <223> Xaa = ANY AMINO ACID

<400> 46
 Gly Phe Met Glu Val Gln Leu Val Lys Ala Lys Glu Leu Cys Asp Thr
 1 5 10 15
 Asp Phe Phe Gly Ser Met Asp Pro Tyr Val Val Ile Gln Tyr Asn Gly
 20 25 30
 Gln Glu Gln Arg Ser Ser Val Ala Lys Gly Gln Gly Asn Asn Pro Val
 35 40 45
 Trp Asn Glu Lys Phe Val Phe Lys Val Glu Tyr Pro Thr Leu Ser Asn
 50 55 60
 Ser Tyr Lys Ile Ile Leu Xaa Ile Met Asp Lys Asp Leu Leu Ser Ala
 65 70 75 80
 Asp Asp Phe Val Gly Gln Ala Ile Val
 85

<210> 47
 <211> 473
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (296)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (473)
 <223> n=a,c,g or t

<400> 47
 tccaaacgcg acctcatcag agcaagaccc ggaggaaaca aggagaggcc agagcggcct 60
 gtcacaaggc aaggacagag gaggtgcttg ttcaggtctc ctgctagatc cggaggcgat 120
 gggcaggggc tgctggaggt gcatctcgtc gacgccaagg gcctcttcgg cagcgatttc 180

ctaggaagat cgacccgtat gtaatcgtgc aataccggag ccaggagcgc aagagcagca 240
ctccagagat gaggggagga acccgagctg gaacgaggtg ttccgggtcc agatcnctcc 300
tctgcgggcca acgggcagca caagctcttc ctccggatca tggaccacga catcttctcc 360
agcgacgact tctcgggcca agcgacgac aacgtgaccg atctgatcag accggcatgg 420
agaagcgggc gcgtcgcagc tgaacgcggc aaagtacaac gttgtgtgcc gcg 473

<210> 48
<211> 99
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (24)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (47)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (62)
<223> Xaa = ANY AMINO ACID

<400> 48
Gly Gln Gly Leu Leu Glu Val His Leu Val Asp Ala Lys Gly Leu Phe
1 5 10 15
Gly Ser Asp Phe Leu Gly Arg Xaa Asp Pro Tyr Val Ile Val Gln Tyr
20 25 30
Arg Ser Gln Glu Arg Lys Ser Ser Thr Pro Glu Met Arg Gly Xaa Gly
35 40 45
Glu Glu Pro Glu Leu Glu Arg Gly Val Pro Val Pro Asp Xaa Ser Ser
50 55 60
Ala Ala Asn Gly Gln His Lys Leu Phe Leu Arg Ile Met Asp His Asp
65 70 75 80
Ile Phe Ser Ser Asp Asp Phe Leu Gly Gln Ala Thr Ile Asn Val Thr
85 90 95
Asp Leu Ile

<210> 49
<211> 465
<212> DNA
<213> Oryza sativa

<400> 49
aaagatcacc caaaacccta tattccatag ttgagacaca agattttttg aagccaagtt 60
tgcgcattac atcaaagggt tcttttgatg cgaccaatgc tgtgaagagt gtaactagca 120
gtatctctag cgcttcaggg aagcatgtcg ctgacgatac aagagaattt gttggagagc 180
tgaacattac agtggttaaga ggtattcaag ttggcgcgtca gagacatgct aacgagcgat 240
ccatatgttg ttctaacact tggggagcag aaagctcaaa ccactgttaa accgagtgc 300
ttgaacccag tatggaatga ggtgcttaag atatcaattc ctcgaaatta tggacctctt 360
aaacttgaag tatacgacca tgatacgttc tctgctgatg atatcatggg ggaagcggag 420
atagatcttc aaccaatgat cacagccgtc atggcctttg gagaa 465

<210> 50
<211> 31
<212> PRT

<213> Oryza sativa

<400> 50

Val Val Leu Thr Leu Gly Glu Gln Lys Ala Gln Thr Thr Val Lys Pro
1 5 10 15

Ser Asp Leu Asn Pro Val Trp Asn Glu Val Leu Lys Ile Ser Ile
20 25 30

<210> 51

<211> 390

<212> DNA

<213> Oryza sativa

<220>

<221> unsure

<222> (43)

<223> n=a,c,g or t

<220>

<221> unsure

<222> (204)

<223> n=a,c,g or t

<220>

<221> unsure

<222> (301)

<223> n=a,c,g or t

<220>

<221> unsure

<222> (347)

<223> n=a,c,g or t

<220>

<221> unsure

<222> (373)

<223> n=a,c,g or t

<400> 51

gcctgtgcaa catcatcatc aagaagaaga agagatcaac ggnaagaaga ctagcgacta 60
gagagagatc gatcgaagag aagaggagag atgggtgcacg ggaagctgga ggtcctcctc 120
gtctgcgcca agggcctcga ggacactgac ttcttgaacg acatggaccc ctacgtgatc 180
ctcacctgcc gcactcagga gcangaaaag cagcgttgca aaaggagcag gaagcgagcc 240
tgaatggaac gagaccttcg tcttcaccgt ctccgacgat gttccacagc tcaatgtcaa 300
ngatcatgga caagtgatgg ccttctcaag ctgacgattt cggtcnngt gaagcaaaca 360
attcctctgg gangcctgtg ttctctggaa 390

<210> 52

<211> 69

<212> PRT

<213> Oryza sativa

<400> 52

Met Val His Gly Lys Leu Glu Val Leu Leu Val Cys Ala Lys Gly Leu
1 5 10 15

Glu Asp Thr Asp Phe Leu Asn Asp Met Asp Pro Tyr Val Ile Leu Thr
20 25 30

Cys Arg Thr Gln Glu Gln Lys Ser Ser Val Ala Lys Gly Ala Gly Ser
35 40 45

Glu Pro Glu Trp Asn Glu Thr Phe Val Phe Thr Val Ser Asp Asp Val
50 55 60

Pro Gln Leu Asn Val
65

<210> 53
<211> 489
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (417)
<223> n=a,c,g or t

<220>
<221> unsure
<222> (428)
<223> n=a,c,g or t

<220>
<221> unsure
<222> (452)
<223> n=a,c,g or t

<220>
<221> unsure
<222> (482)
<223> n=a,c,g or t

<400> 53
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catttctggc acaatttttt ccacctttat ttcaacttta agactccaca gaaagaagca 120
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Asp Asp Asn Asp Phe Leu Ser Ser Ile Asp Pro Tyr Val Ile Leu Thr
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Tyr Arg Ala Gln Glu Lys Lys Ser Thr Val
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